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1/24

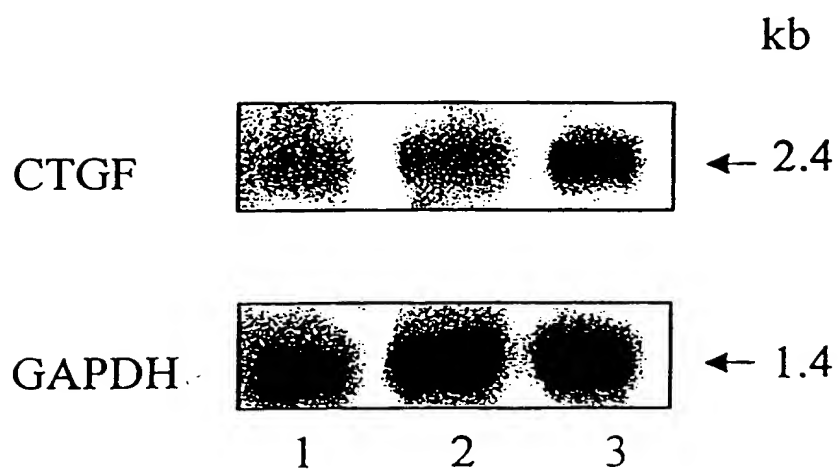


Fig. 1

2/24

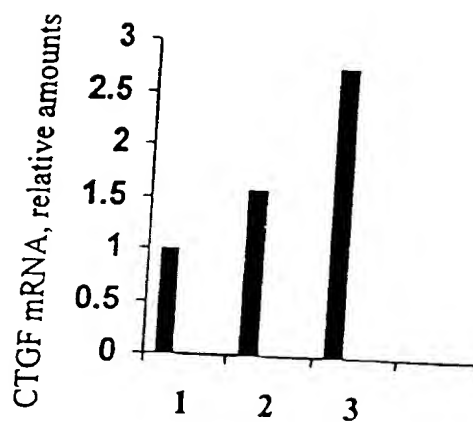


Fig. 2

3/24

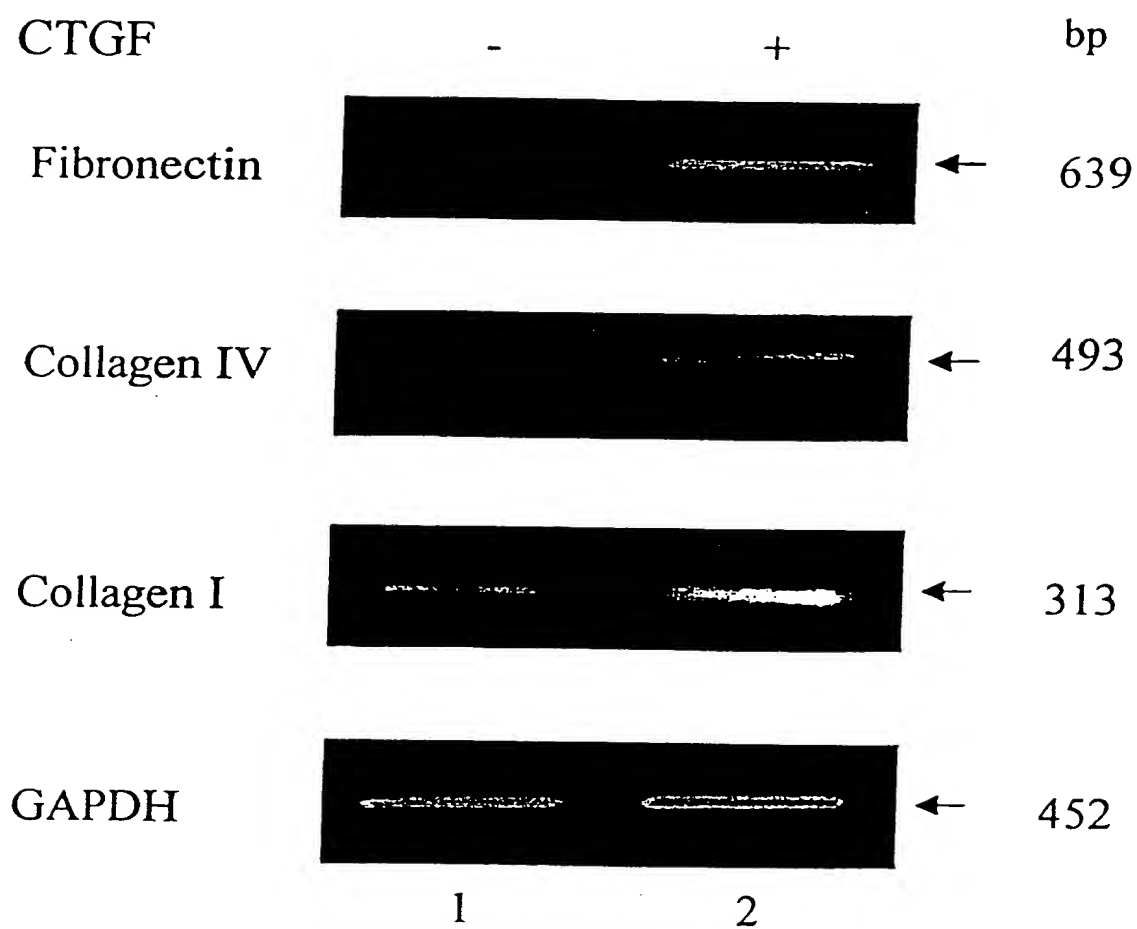


Fig. 3

4/24

rat: 1 atctccacccgGgttaccaatgacaatacTttctgcagGctggagaagcagagTcgTctc 60
 mouse: 783 atctccacccgagt taccaatgacaataccttctgcagactggagaagcagagccgcctc 842

rat: 61 tgcattggtcaggccctgTgaagctgacctAgaggaaaacattaagaagggcaaaaagtgc 120
 mouse: 843 tgcattggtcaggccctgcgaagctgacctggaggaaaacattaagaagggcaaaaagtgc 902

rat: 121 atccggacGcctaaaatTgccaagcctgtcaagtttgagctttctggctgcaccagtgtg 180
 mouse: 903 atccggacacctaataatcgccaagcctgtcaagtttgagctttctggctgcaccagtgtg 962

rat: 181 aagacCtacCgggctaagttctgTgggggtgtgcacGgacggccgctgctgcacaccgcac 240
 mouse: 963 aagacatacagggctaagttctgcggggtgtgcacagacggccgctgctgcacaccgcac 1022

rat: 241 agaaccaccacActgccggtggagttcaaGtgccccCatggcgaAatcatgaaaaagaac 300
 mouse: 1023 agaaccaccactctgccagtggagttcaaagccccgatggcgagatcatgaaaaagaat 1082

rat: 301 atgatgttcatcaagacctgtgcctgccattacaactgtcc 341 (SEQ ID NO: 29)
 mouse: 1083 atgatgttcatcaagacctgtgcctgccattacaactgtcc 112 (SEQ ID NO: 30)

Fig. 4

5/24

rat: 1 ISTRVTNDNTFCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKIAKPVKFELSGCTSV 180
mouse: 216 ISTRVTNDNTFCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKIAKPVKFELSGCTSV 275

rat: 181 KTYRAKFCGVCTDGRCCCTPHRTTTLPVEFKCPHGEIMKKKNMMFIKTCACHYNC 339 (SEQ ID NO: 31)
mouse: 276 KTYRAKFCGVCTDGRCCCTPHRTTTLPVEFKCPDGEIMKKKNMMFIKTCACHYNC 328 (SEQ ID NO: 32)

Fig. 5

6/24

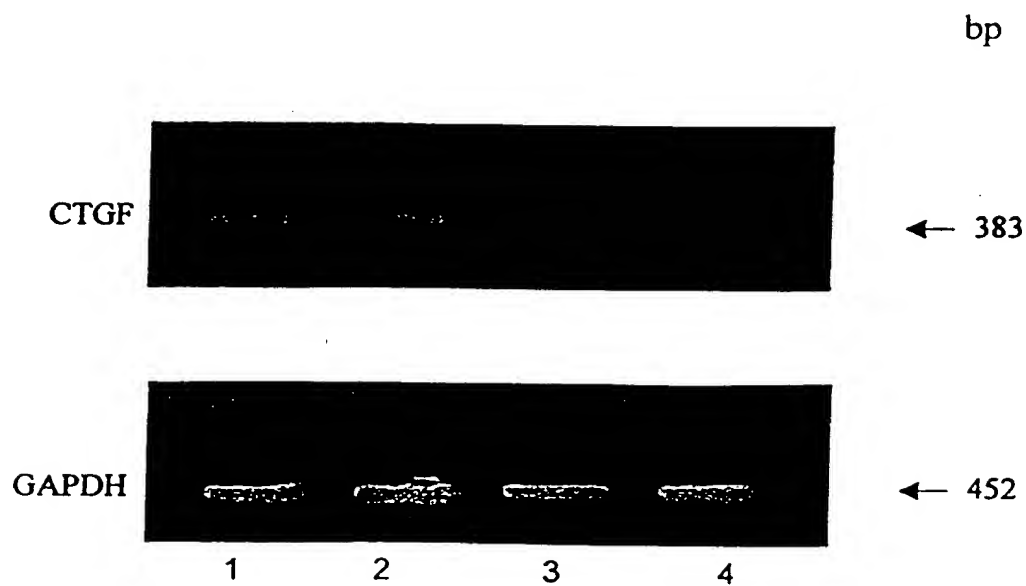


Fig. 6

7/24

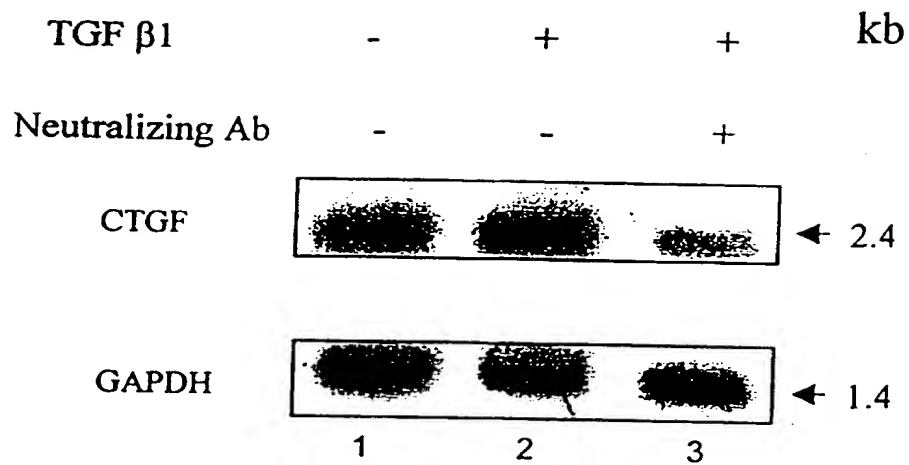


Fig. 7

8/24

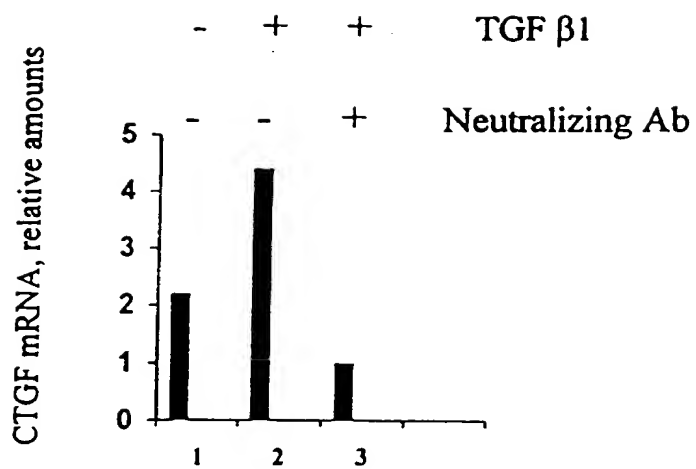


Fig. 8

9/24

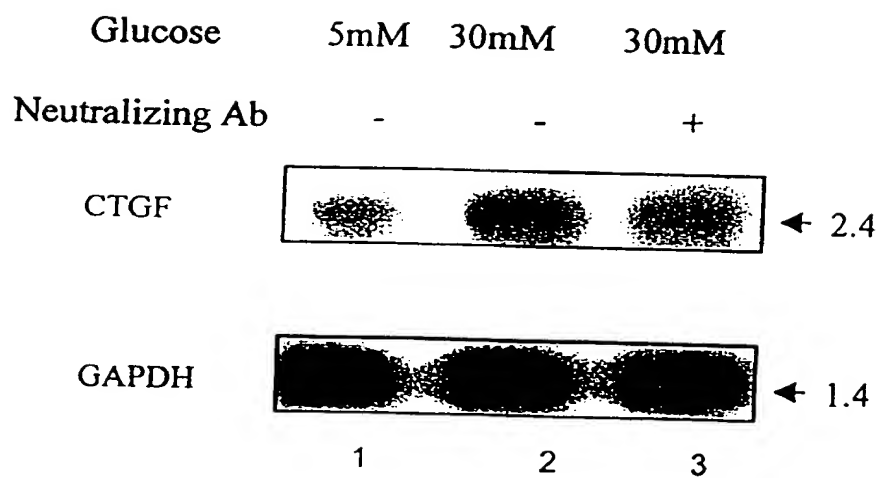


Fig. 9

10/24

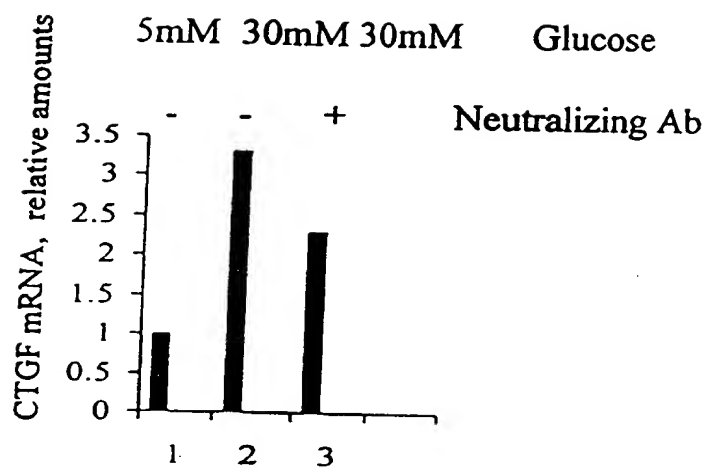


Fig. 10

11/24

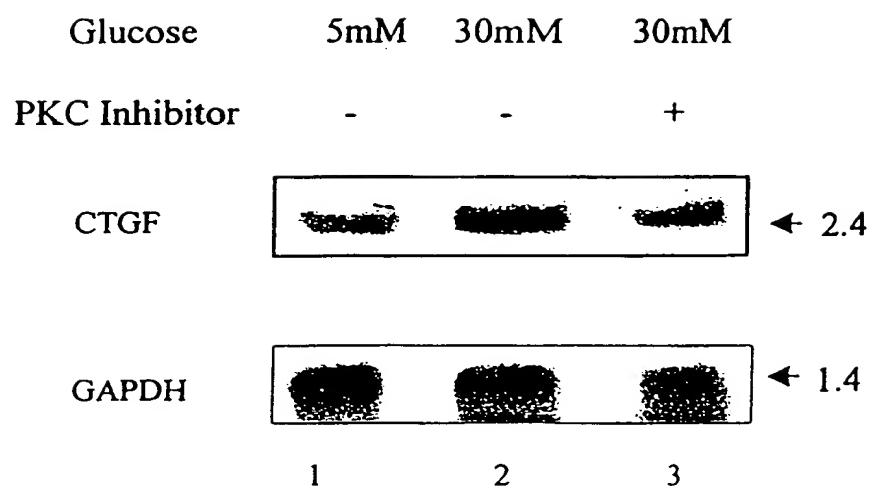


Fig. 11

12/24

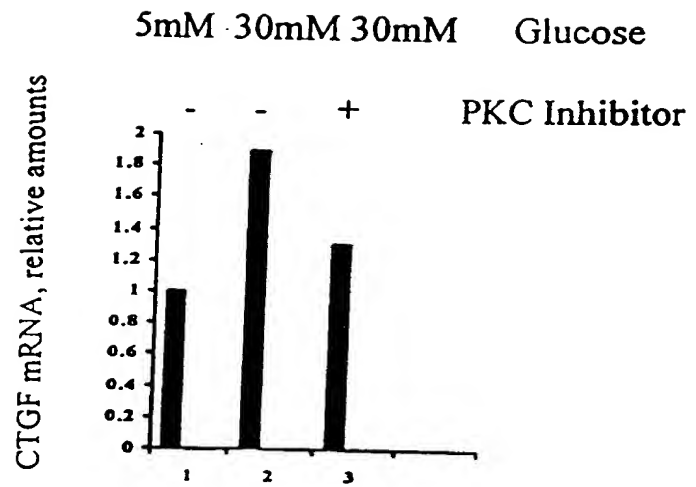


Fig. 12

13/24

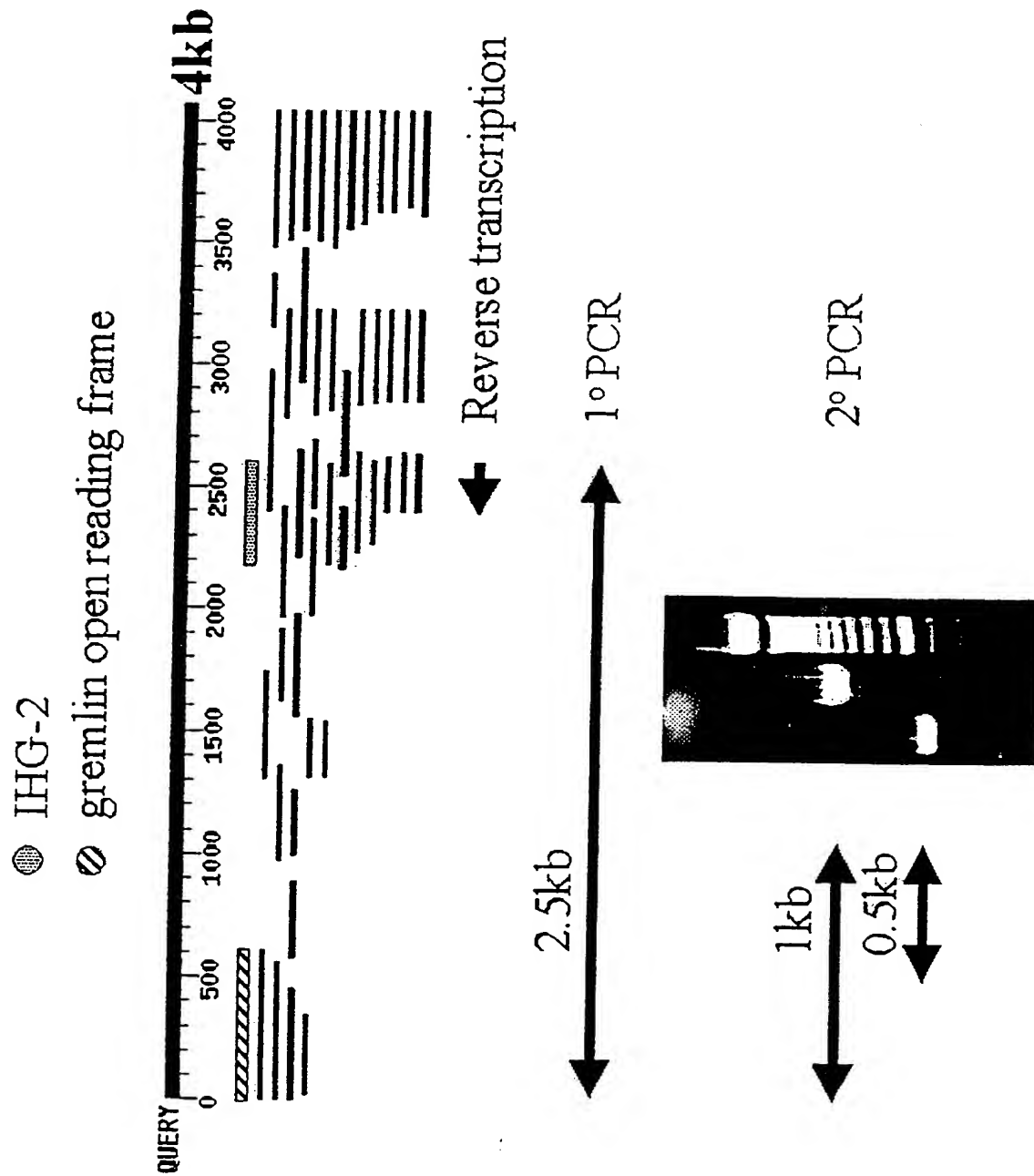
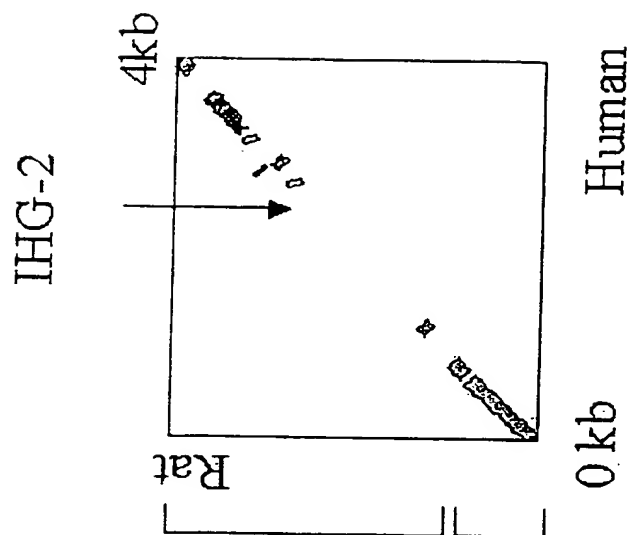


Fig. 13

14/24



3' Untranslated

Open Reading Frame

Fig. 14

15/24

1 CGCGCCGCACTCAGCGCCACGCGTCGAAAGCGCAGGCCCCGAGGACC CGCGCACTGACAGTATGAGCCGCACAG
M S R T A
76 CCTACACGGTGGGAGCCCTGCTTCTCCTCTTGGGACCCTGCTGCGGGCTGCTGAAGGAAAAAGAAAGGGTCCC
Y T V G A L L L L L G T L L P A A E G K K G S Q
151 AAGGTGCCATCCCCCGCCAGCAGAGGCCAGCAATGACTCAGACGACAGTCACTGCCCCAGCAGCCTGGCT
G A I P P P D K A Q H N D S E Q T Q S P Q Q P G S
226 CCAGGAACCGGGGCGGGGCCAAGGGCGGGGCACTGCCATGCCGGGGAGGAGGTGCTGGAGTCCAGCCAAGAGG
R N R G R G Q G R G T A M P G E E V L E S S Q E A
301 CCCTCGATGTGACGGAGCGCAAATACCTGAAGCGAGTGTGCAAAACCCAGCCGCTTAAGCAGACCATCCACG
L H V T E R K Y L K R D W C K T Q P L K Q T I H E
376 AGGAAGGCTGCAACAGTCGCACCATCATCAACCGCTTCTGTTACGGCCAGTGAACATCTTTCTACATCCCCAGG
E G C N S R T I I N R F C Y G Q C N S F Y I P R H
451 ACATCCGGAAGGAGGAAGGTTCTTTTCTGCTCCTTCTGCAAGCCCAAGAAATCTACATCCATGATGGTCA
I R K E E G S F Q S C S F A C K P K K F T T M M V T
526 CACTCAACTGCCCTGACACGACCTACCAAGAAGAAGAGTACACAGTGGAAGCAGTGTCTGTCATAT
L N C P E L Q P P T K K K R V R V K Q C R C I S
601 CCATCGATTGGTGAATTAAGCCAAATCCAGGTGCACCCAGCATGTCTAGGAATGCAGCCCCAGGAAGTCCCAGACC
I D L D
676 TAAACAACCCAGATTCTTACTTGGCTTAAACCTAGAGGCCAGAAGAACCCCGAGTGCCTCCTGGCAGGAGCCTG
751 CTGTGCGTAGTTCGTGTGCATGAGTGTGATGGGTGCCTGTGGGTGTTTTAGACACCAGAGAAAAACACAGTCT
826 CTGCTAGAGAGCACTCCCTATTTTGAACATATCTGCTTTAATGGGGATGTACACAGAAACCCCTCCACCCCG
901 CTCACATCTAAAGGGGCGGGGCGGTGCTTGGTTCTGACTTTGTGTTTTGTGGCTCCTGGGAGCCAGAAATCTC
976 TTTTCGGAATGAATGTTTCATGGAAGAGGCTCCTCTGAGGGCAAGAGACCTGTTTTAGTGCTGCATTTCGACATGGA
1051 AAAGTCCTTTTAACTGTGCTGCTCATCTCTCTCTCTCTCTCTCTCAACTCAATCTCTCTTTCTTAAGTTGATAGT
1126 GACTATGTTCAGTCTTAATCTCTTGTGTCGAAGGTTCCTAAATTAATTCATTAACCATGAATGCAAAATGTTTTCA
1201 TTTTGTGAAGACCCCTCCAGACTCTGGGAGAGGCTGGTGTGGGCAAGGACAAGCAGGATAGTGGAGTGAGAAAGGG
1276 AGGGTGGAGGCTGAGGCCAAATCAGGTCCAGCAAAAGTCAGTAGGGACATTCGCAAGCTTTGAAAGGCCAATACC
1351 AGAACACAGGCTGAGTCTCTGAGAAAGTCTTTCTAGTATTTAACAGAACCCAGTAGGACGAGGAGGAATGA
1426 GATTGCCAGAAAGTGATTAATCTTTGGCCGTTGCAATCTGCTCAAACTTAACACAACTGAAACATAAAATCTG
1501 ACCACTCCTATGTTCCGACCCCAAGCAAGTTAGTAAACCAAACTCCCTGCTGTTGTCCTCAGGTGGGAAAA
1576 GACAGGTGATTTAGAACTCTGCATAGGGGTGGGAATTAACAAAACCKAGAGCTGGAAATTCCTAATCACT
1651 TTCCTTTATCGTGGTTATAGTCAGCTCATTTCCTATCCACTATTTCCCATATGCTTCTGAGAGCCACTAATCTG
1726 ATTGATAAAGATCTGCCTCTGCTGAGTGTACCTGACAGTAAGTCTAAGAGTAGARAGATTTAGGGACTACTCTG
1801 TTTTAGCAAGARATATTTGGGGGCTCTTTTGTGTTTAACTATTTGACAGAGATTGGCTARAGAGAAGACGCA
1876 GAGTAAGGAAATAAAGGGRATTGCCCTCTGGCTAGAGAGTAAGTTAGGTGTTAATACCTGGTAGAAATGTAAGGGA
1951 TATGACCTCCCTTTCTTTATGTGCTCAGTAGGATCTGAGGGAGCCCTGTTAGGAGAGCATAGCATCATGATGTA
2026 TAGCTGTTCACTCTGCTAGTGGTGGATGGACATAACTATTTGTAATCTAGTATTTACTGGTAGGCATGTCC
2101 TCTGATTAACCTTGGCCTACTGGCAATGGCTACTTAGGATTGATCTAAGGGCCAAAGTCAGGGGTGGTGAATCT
2176 TATTCTACTTTGGATTGGTTAACTGTTTCTTCAAGCTGAGGTTTTATATCAAACTCCCTGAATACTCTTT
2251 TTGCCTGTATCTTCTCAGGCTCCTAGGCAAGTCTCATGTAATGGAACCAAACTGCAGACTGCAGACTTGATCTTA
2326 GTTGCCGATCAAGGCTCTGGCATTACAGAGAACCCTTCAACTCGAGAAGCTGTTTTATTCTGTTTTGTTTTGA
2401 TCCAGTGCTCTCCCATCTAAACACTAAACAGGAGGACATTTCAAGGCGGAGATATTTAAACACCCAAATGTTG
2476 GGTCTGATTTTCAAACTTTTAACTCACTAGTATGATTTCTACGCTGAGCGAATTTGTCBAAACBACATAGTGTG
2551 TGTGTTTTGTATACACTGTATGACCCACCCCAAACTCTGTGATTTGCTTCAACTTCCACATAAAGCAGAGAG
2626 TGGATTTAATTAAGCACAATAAGTCTAAGGCGAAATTTGAGGGTGGGAGAGAAGAAAGGAAAGAGCTGAAA
2701 ATGTAACACACACAGGAGGAAAAATGACATTCAGAACCCAGCAACATGAAATCTCTTGTGTTTAACTC
2776 TGCCACAAGAATGCAATTCGTTAATGAGATGACTTAAGTTGGCAGCAGTAATCTCTTTTAGGCGTTGATCC
2851 ACAGTCTTGACATTAAGTGAGATTTGGCTCAAGTAAAGAGAATTTCTCAACCTAATCTCACTGGGATAATCA
2926 GCAGCGTATACCTCCCTAAAGCATATCACTAGCCAAAGAGGAAATATCTGTTCTTCTTACTGTGCTATATTA
3001 GACTAGTACAAATGGTGTGCTTCAAGTTTCAATGAAATGCCATATCTATACCATTTTATTCGATGCAC
3076 TGATGATGTAATGATATATTTTTTCATTATATAGTAGAATATTTTTATGGCAAGATATTTGTGGTCTTGATCAT
3151 ACCTATTAATAATGCCAAACCAAAATGAAATTTATGATGTACACTTTGTGCTTGGCATTAAGAAAGAAAA
3226 ACACATCTCCGGAAGTCTGAAGTGTGTTTTTGTGTTACTGTAGGTCCTCAAAGTAAAGAGTGAAGTGAATAATC
3301 TGGAGGAGAGGATAATTTCCACTGTGTGGAATGTGAATAGTTAAATGAAAAGTTATGGTTATTTAATGTAATTA
3376 TACTTCAATCCTTTGGTCACTGTGATTTCAAGATGTTTTCTTTTTCTTTTATAGCATCTTCTCTGAGTTGG
3451 CGAAAGAAGAGCTGACACACCGTATGTTGTTAGAGTCTTTATCTGGTGGAGGAAACAAATCTTGACCCAG
3526 TGAACATGTCTTCTGAGTCAGTGCCTGAATCTTTATTTTTAAATGGAATGTTCTTAAAGGTTAACTTTCTA
3601 AAGCAATATTAAGAAAGACTTTAAATGTTATTTTGGAAAGCTACGATGCATGATACAAACGAATAGCAGATAA
3676 TGATGACTAGTTCACACATAAAGCTTTTAAAGGAAAACTAAATGAAAGTGGATAAACAGAACTTTATA
3751 AGTGATCAGTTAATGCCTAAGAGTGAAAGTAGTTCTATTGACATTCCTCAAGATTTAATATCAACTGCATTA
3826 GTATTATGTCTGCTTAATCATTTAAAAACGGAAAGATTAATAGACATGAGGTACCTTGCTGTGAGGAGG
3901 ATGAAGGGGAGTTGATAGTCTCATAAACTAATTTGGCTTCAAGTTTCATGAATCTGTAAGTGAATTTAATTT
3976 TCACCCCAATAATGTTCTATATAGCCTTTGCTAAAGAGCACTAATAAATTAACCTATGCTTTCAAAAAA

(SEQ ID NO: 33)

Fig. 15

16/24

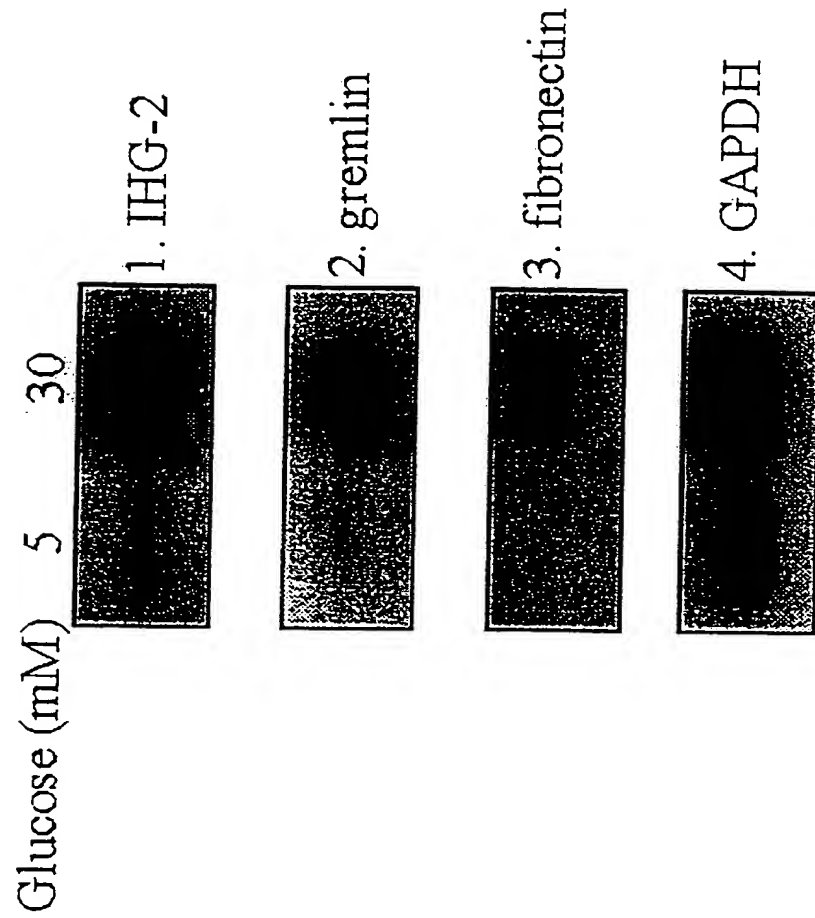


FIG. 16

17/24

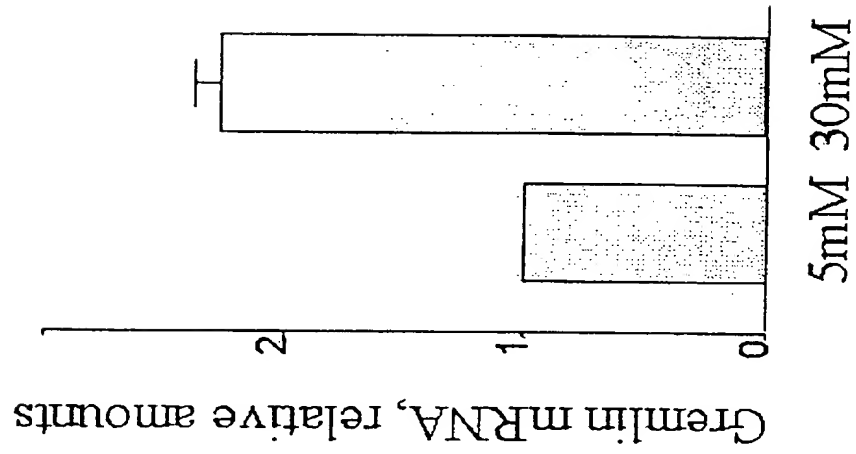


FIG. 17

18/24

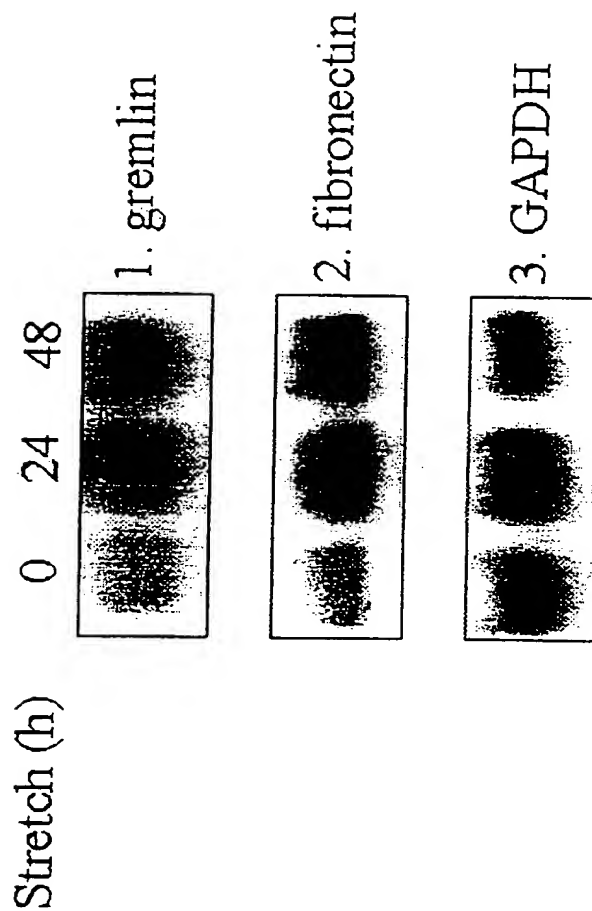


FIG. 18

19/24

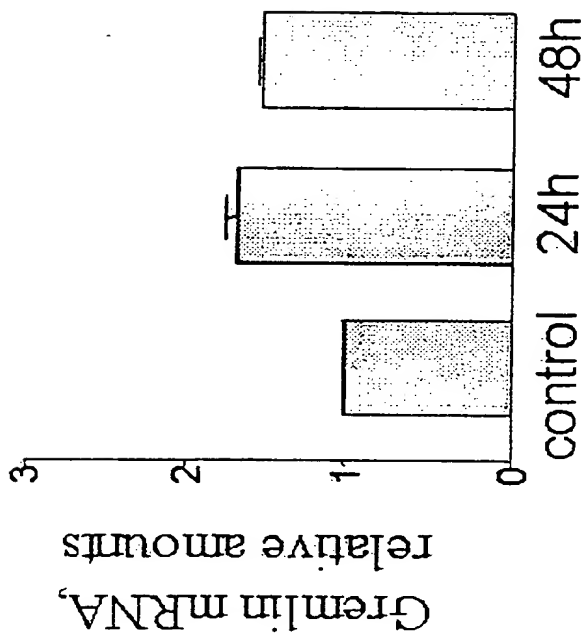


FIG. 19

20/24

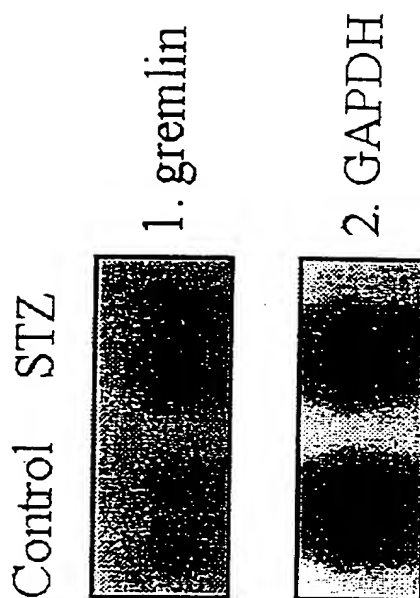


FIG. 20

21/24

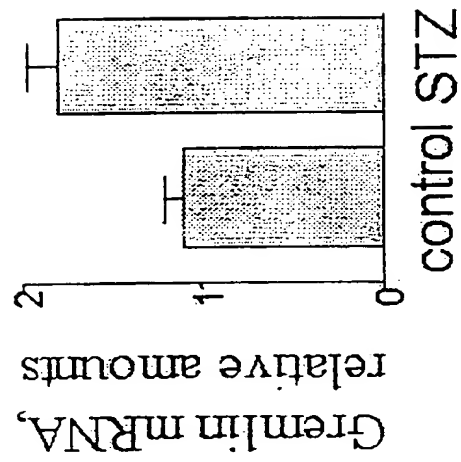


FIG. 21

22/24

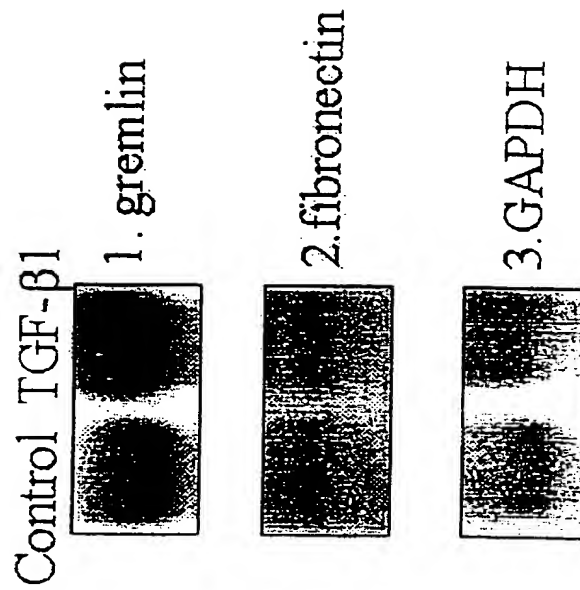


Fig. 22

23/24

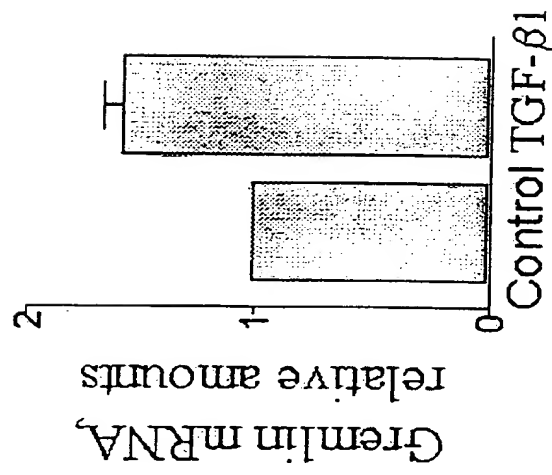


Fig. 23

24/24

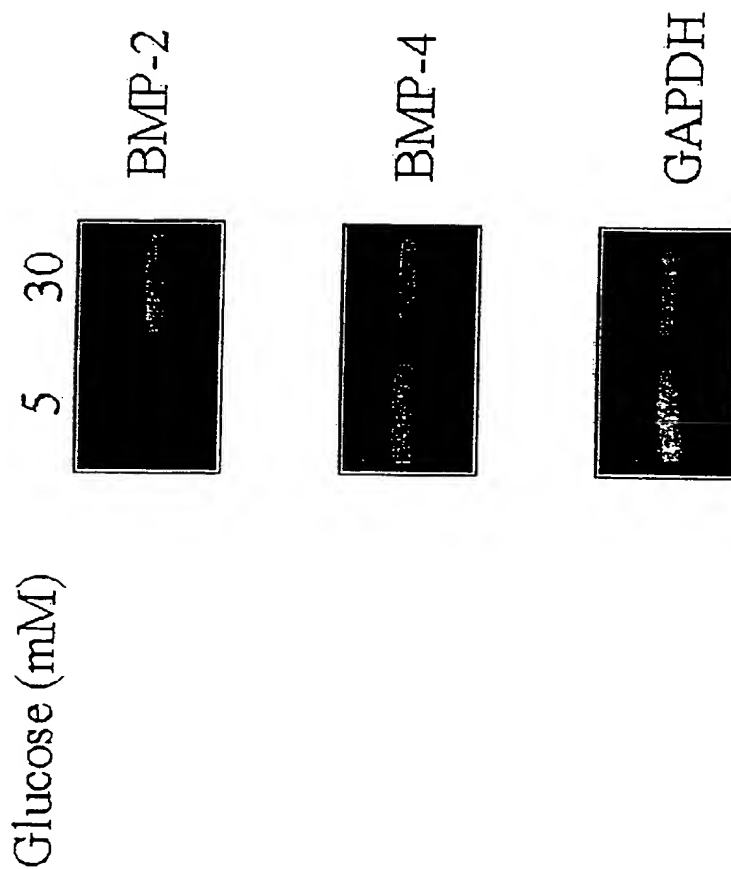


Fig. 24